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Sequence length 3637

GTGACCCACGCGTCCGCACTCAACAATGCCTGCCCCCTCTCTGACTGCACCGTCCCGCCGCGCTGCCGCCGCCGCCGCC	79
CAAGCCAAGTCGAGCGGGGGCGTTGCCACCCGACGGCACAGCCCTTGGGCCCGCCCGGGACCAGGAGGTGAGCCGCGCG	158
CGCACAGCTCCGTGCGCTCGCCCGTCTGAGCGCCCCGCCAGGTGCCCGCAGCCCGCCGCCGAG	233
ATG CAC AGC CCG	4
P G L L A L W L C A V L C A S A R G G S	24
CCT GGG CTC CTG GCG CTG TGG CTT TGC GCT GTG CTG TGC GCA TCG GCG CGC GGG GGC AGC	293
D P Q P G P G R P A C P A P C H C Q E D	44
GAC CCC CAG CCT GGC CCG GGG CGT CCC GCC TGC CCG GCT CCC TGC CAC TGC CAG GAG GAC	353
G I M L S A D C S E L G L S V V P A D L	64
GGC ATC ATG CTG TCC GCT GAC TGC TCC GAG CTC GGG CTC TCA GTG GTG CCT GCG GAC CTG	413
D P L T A Y L D L S M N N L T E L Q P G	84
GAC CCC CTG ACG GCT TAC CTA GAC CTC AGT ATG AAC AAC CTC ACG GAG CTT CAG CCG GGT	473
L F H H L R F L E E L R L S G N H L S H	104
CTC TTC CAC CAC CTG CGC TTC CTG GAG GAG CTG CGG CTC TCA GGG AAC CAC CTC TCA CAC	533
I P G Q A F S G L H S L K I L M L Q S N	124
ATC CCG GGA CAG GCA TTC TCC GGC CTC CAC AGC CTC AAA ATT CTA ATG CTG CAG AGC AAC	593
Q L R G I P A E A L W E L P S L Q S L R	144
CAG CTC CGT GGG ATC CCA GCA GAG GCA CTA TGG GAG CTG CCC AGC CTG CAG TCG CTG CGC	653
L D A N L I S L V P E R S F E G L S S L	164
CTA GAT GCT AAT CTC ATC TCC CTG GTC CCT GAG AGA AGC TTT GAG GGG CTC TCC TCC CTC	713
R H L W L D D N A L T E I P V R A L N N	184
CGC CAC CTC TGG CTG GAT GAC AAT GCA CTC ACT GAG ATC CCC GTC AGA GCT CTC AAC AAC	773
L P A L Q A M T L A L N H I R H I P D Y	204
CTT CCT GCC CTA CAG GCC ATG ACC TTG GCT CTC AAC CAT ATC CGC CAC ATC CCT GAC TAT	833
A F Q N L T S L V V L H L H N N R I Q H	224
GCC TTC CAG AAC CTC ACC AGT CTT GTG GTG CTG CAT CTA CAT AAC AAC CGC ATC CAG CAT	893
V G T H S F E G L H N L E T L D L N Y N	244
GTG GGG ACC CAC AGC TTC GAG GGG CTG CAC AAT CTG GAG ACA CTA GAC CTG AAC TAT AAT	953
E L Q E F P L A I R T L G R L Q E L G F	264
GAG CTG CAG GAG TTC CCC TTG GCT ATC CGG ACC CTG GGC AGG CTG CAG GAA TTG GGT TTC	1013
H N N N I K A I P E K A F M G N P L L Q	284
CAT AAC AAC AAC ATC AAG GCT ATC CCA GAG AAA GCC TTC ATG GGC AAC CCT CTC CTG CAG	1073
T I H F Y D N P I Q F V G R S A F Q Y L	304
ACA ATA CAT TTT TAT GAC AAC CCA ATC CAG TTT GTG GGA AGG TCA GCA TTC CAG TAC CTG	1133
S K L H T L S L N G A T D I Q E F P D L	324
TCT AAA CTG CAT ACG CTA TCT TTG AAT GGT GCC ACT GAT ATC CAA GAG TTC CCA GAC CTC	1193
K G T T S L E I L T L T R A G I R L L P	344
AAA GGC ACC ACT AGC CTG GAG ATC CTG ACC CTG ACC CGT GCG GGC ATC AGA CTG CTC CCA	1253

Figure 1

P	G	V	C	Q	Q	L	P	R	L	R	I	L	E	L	S	H	N	V	I	364
CCG	GGA	GTG	TGC	CAA	CAG	CTG	CCT	AGG	CTC	CGA	ATC	CTG	GAG	CTG	TCT	CAT	AAT	CAG	ATC	1313
E	E	L	P	S	L	H	R	C	Q	K	L	E	E	I	G	L	R	H	N	384
GAG	GAG	TTA	CCC	AGC	CTG	CAC	AGA	TGT	CAG	AAG	CTG	GAG	GAA	ATT	GGC	CTC	CGA	CAT	AAC	1373
R	I	K	E	I	G	A	D	T	F	S	Q	L	G	S	L	Q	A	L	D	404
AGG	ATC	AAG	GAA	ATT	GGT	GCA	GAT	ACC	TTC	AGC	CAG	CTG	GGC	TCC	TTG	CAA	GCT	TTA	GAC	1433
L	S	W	N	A	I	R	A	I	H	P	E	A	F	S	T	L	R	S	L	424
CTG	AGT	TGG	AAT	GCC	ATC	CGT	GCC	ATC	CAC	CCT	GAG	GCT	TTC	TCA	ACC	CTT	CGA	TCC	TTG	1493
V	K	L	D	L	T	D	N	Q	L	T	T	L	P	L	A	G	L	G	G	444
GTT	AAG	CTG	GAC	CTG	ACT	GAC	AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGG	CTG	GGA	GGC	1553
L	M	H	L	K	L	K	G	N	L	A	L	S	Q	A	F	S	K	D	S	464
CTG	ATG	CAC	CTG	AAG	CTC	AAA	GGG	AAC	TTG	GCC	CTG	TCT	CAG	GCC	TTC	TCC	AAG	GAC	AGT	1613
F	P	K	L	R	I	L	E	V	P	Y	A	Y	Q	C	C	A	Y	G	I	484
TTC	CCA	AAA	CTG	AGG	ATC	CTG	GAG	GTG	CCC	TAC	GCC	TAC	CAG	TGC	TGT	GCC	TAC	GGC	ATC	1673
C	A	S	F	F	K	T	S	G	Q	W	Q	A	E	D	F	H	P	E	E	504
TGT	GCC	AGC	TTT	TTT	AAG	ACC	TCT	GGG	CAG	TGG	CAG	GCC	GAG	GAC	TTT	CAT	CCA	GAA	GAA	1733
E	E	A	P	K	R	P	L	G	L	L	A	G	Q	A	E	N	H	Y	D	524
GAG	GAG	GCA	CCA	AAG	AGG	CCC	CTG	GGT	CTC	CTT	GCT	GGA	CAA	GCT	GAG	AAC	CAC	TAT	GAC	1793
L	D	L	D	E	L	Q	M	G	T	E	D	S	K	P	N	P	S	V	Q	544
CTA	GAC	CTG	GAT	GAG	CTC	CAG	ATG	GGG	ACA	GAG	GAC	TCA	AAG	CCA	AAC	CCC	AGT	GTC	CAG	1853
C	S	P	V	P	G	P	F	K	P	C	E	H	L	F	E	S	W	G	I	564
TGC	AGC	CCT	GTT	CCA	GGC	CCC	TTC	AAG	CCC	TGC	GAG	CAC	CTC	TTT	GAG	AGC	TGG	GGC	ATC	1913
R	L	A	V	W	A	I	V	L	L	S	V	L	C	N	G	L	V	L	L	584
CGC	CTT	GCT	GTG	TGG	GCC	ATC	GTG	CTG	CTC	TCC	GTA	CTC	TGT	AAC	GGG	CTG	GTG	CTG	CTG	1973
T	V	F	A	S	G	P	S	P	L	S	P	V	K	L	V	V	G	A	M	604
ACA	GTC	TTT	GCC	AGC	GGA	CCC	AGC	CCG	CTG	TCC	CCC	GTC	AAG	CTT	GTG	GTG	GGT	GCG	ATG	2033
A	G	A	N	A	L	T	G	I	S	C	G	L	L	A	S	V	D	A	L	624
GCA	GGC	GCC	AAC	GCC	CTG	ACG	GGC	ATT	TCC	TGT	GGT	CTC	CTG	GCC	TCT	GTG	GAC	GCC	TTG	2093
T	Y	G	Q	F	A	E	Y	G	A	R	W	E	S	G	L	G	C	Q	A	644
ACC	TAT	GGT	CAG	TTC	GCT	GAG	TAT	GGA	GCC	CGC	TGG	GAG	AGC	GGT	CTG	GGC	TGC	CAG	GCT	2153
T	G	F	L	A	V	L	G	S	E	A	S	V	L	L	L	T	L	A	A	664
ACG	GGC	TTC	CTG	GCT	GTC	CTG	GGT	TCA	GAG	GCG	TCG	GTG	CTG	CTG	CTC	ACA	CTG	GCG	GCC	2213
V	Q	C	S	I	S	V	T	C	V	R	A	Y	G	K	A	P	S	P	G	684
GTG	CAG	TGC	AGC	ATC	TCT	GTG	ACC	TGC	GTC	CGA	GCC	TAC	GGG	AAG	GCG	CCG	TCG	CCT	GGC	2273
S	V	R	A	G	A	L	G	C	L	A	L	A	G	L	A	A	A	L	P	704
AGC	GTC	CGC	GCA	GGC	GCA	CTG	GGA	TGC	CTG	GCG	CTG	GCC	GGG	CTG	GCC	GCA	GCA	CTG	CCG	2333
L	A	S	V	G	E	Y	G	A	S	P	L	C	L	P	Y	A	P	P	E	724
CTG	GCC	TCG	GTG	GGA	GAG	TAT	GGC	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCC	CCA	CCC	GAG	2393
G	R	P	A	A	L	G	F	A	V	A	L	V	M	M	N	S	L	C	F	744
GGC	CGG	CCG	GCC	GCC	CTG	GGC	TTC	GCT	GTA	GCC	CTG	GTG	ATG	ATG	AAC	TCG	CTC	TGC	TTC	2453

Figure 1 (Cont'd)

L V V A G A Y I K L Y C D L P R G D F E	764
CTG GTG GTG GCC GGC GCC TAC ATC AAG CTC TAC TGT GAC CTG CCA CGG GGT GAC TTT GAG	2513
A V W D C A M V R H V A W L I F A D G L	784
GCC GTG TGG GAC TGC GCC ATG GTG CGC CAC GTG GCC TGG CTC ATC TTT GCA GAT GGC CTC	2573
L Y C P V A F L S F A S M L G L F P V T	804
CTC TAC TGC CCC GTG GCC TTC CTC AGC TTT GCC TCC ATG CTG GGC CTC TTC CCT GTC ACC	2633
P E A V K S V L L V V L P L P A C L N P	824
CCC GAG GCT GTC AAG TCA GTC CTT CTG GTG GTG CTG CCT CTG CCT GCC TGC CTC AAC CCA	2693
L L Y L L F N P H F R D D L R R L W P S	844
CTG CTC TAC CTG CTC TTC AAC CCT CAC TTC CGG GAT GAC CTT CGG CGG CTC TGG CCA AGC	2753
P R S P G P L A Y A A A G E L E K S S C	864
CCT CGG TCC CCA GGG CCC CTA GCC TAC GCT GCA GCC GGT GAG CTG GAG AAG AGC TCC TGC	2813
D S T Q A L V A F S D V D L I L E A S E	884
GAC TCC ACC CAA GCG CTG GTG GCT TTC TCA GAT GTG GAT CTT ATT CTG GAA GCT TCT GAG	2873
A G Q P P G L E T Y G F P S V T L I S R	904
GCT GGG CAG CCT CCT GGG CTA GAG ACC TAT GGC TTC CCT TCA GTG ACC CTC ATC TCC CGA	2933
H Q P G A T R L E G N H F I E S D G T K	924
CAT CAG CCG GGG GCC ACC AGG CTG GAG GGA AAC CAT TTT ATA GAG TCT GAT GGA ACC AAG	2993
F G N P Q P P M K G E L L L K A E G A T	944
TTT GGG AAC CCA CAA CCT CCC ATG AAG GGA GAA CTG CTG CTG AAG GCA GAG GGA GCC ACT	3053
L A G C G S S V G G A L W P S G S L F A	964
TTG GCA GGC TGT GGC TCT TCC GTG GGT GGA GCC CTC TGG CCC TCT GGC TCT CTC TTT GCC	3113
S H L *	968
TCT CAC TTG TAA	3125
ATATCCCTCTCTGTTTGTCTCTCCCCATCCAATGATGGCTGCTTATAAAAGAAAGACAACCTCCAACCTCCATAGCAAGA	3204
TGGCCAACACCTCTGACTCCATTGTTCTCTCTCCACGACCCCTAACCAATGAGTGCTTCCAAGTCTTGCTTTGTCTTGG	3283
CCTTCAGCTTCACTTTACCCCTGGGCCTTCTCTGTCCAATCCAATACCTTCTGACAGAGGCCTGGGAAATTGTCATAGGA	3362
GAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGCCCTGACAGAGCCATGATCAGTAAGTGCAGAGTGATGGGGAG	3441
GTCTCACAGAGCATGACACTGGAAGACAACTACCAAAGACATTGGAGAGTCTCCCTGTGACATATAGAATATAAAATG	3520
TGTTCTGCGTTCCATTAATCTTGACCTATGCTGNGCCAAAGTGCTTCTGTAAAATAACCTTTGGAAGACATTGAAAA	3599
AAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC	3637
??	

Figure 1 (Cont'd)

LRR: domain 1 of 8, from 67 to 114: score 46.0, E = 8.1e-10
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +LdLs N+Lt+I pg++++L+ Leel Ls+N+L+++p ++++L+
 ftmzb048h1
 67 LTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGNHLSHIPGQAFSGLH 114

LRR: domain 2 of 8, from 115 to 162: score 42.2, E = 1.2e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ L L+ N+L+++p++al+ Lp+L++L L+ N ++ +p+++++L+
 ftmzb048h1
 115 SLKILMLQSNQLRGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS 162

LRR: domain 3 of 8, from 163 to 210: score 49.5, E = 7.7e-11
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L++L+L++N Lt++p al+nLp L+ L N+++++p++++fqnl+
 ftmzb048h1
 163 SLRHLWLDDNALTEIPVRALNNLPALQAMTLALNHIRHIPDYAFQNL 210

LRR: domain 4 of 8, from 211 to 257: score 39.5, E = 7.4e-08
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+L+L nN+++++ +++++L+nLe+LdL++N+L+++p ++L+
 ftmzb048h1
 211 SLVVLHLHNNRIQHVGHSTFEGHLNLETLDLNYNELQEFPL-AIRTLG 257

LRR: domain 5 of 8, from 258 to 305: score 34.1, E = 3.2e-06
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+eL + nN+++ +p+ a+ + p L+++++ +N ++ + ++fq L+
 ftmzb048h1
 258 RLQELGFHNNNIKAIEKAFMGNPPLLQTIHFYDNPIQFVGRSAFYLS 305

LRR: domain 6 of 8, from 306 to 352: score 23.8, E = 0.0041
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L++L+L++ +++++p+ I++ ++Le L L + ++ lppg++q L+
 ftmzb048h1
 306 KLHTLSLNGATdIQEFPD-LKGTTSLEILTLTRAGIRLLPPGVCQQLP 352

LRR: domain 7 of 8, from 353 to 398: score 47.6, E = 2.8e-10
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ L+Ls+N++++lp+ I+ +++Lee+ L +N+++++ ++f+ L+
 ftmzb048h1
 353 RLRIELSHNQIEELPS-LHRCQKLEEIGLRHNRIKEIGADTFSQLG 398

LRR: domain 8 of 8, from 399 to 446: score 49.4, E = 7.9e-11
 ->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnlk<-
 +L+ LdLs N ++ ++p+a+s+L++L +LdL +N+Lt+lp + +L
 ftmzb048h1
 399 SLQALDLSWNAIRAIHPEAFSTLRSLVKLDLTDNQLTTLPLAGLGGLM 446

Figure 2

Proteins with leucine-rich repeats

Protein (species) ^a	Function-ligand ^a	Location ^{a,b}	Repeats ^c	Length ^d	Consensus sequence ^e					PIR ^f entry
					5	10	15	20	25	
RNase inhibitor (porcine)	RNase inhibitor-RNase	Cytoplasm	15	28 (A) 29 (B)	.LE.L.L.L.C-.LT...C.L..aL...					A31857
Leucine-rich α2-GP (human)	?-?	Serum	8	24	.L.L.L.L.N-.L..-L.L.L.L..					N8HUA2
RNA1 (Saccharomyces cerevisiae)	RNA processing-?	Cytoplasm	8	29	.L.L.L.L.N-.a.....a.a.....					8VBYN1
U2 snRNP A' (human)	Splicing-U2 snRNP	Nucleus	4	24	.L.L.a.N-.a.....L..					S03616
Biglycan (human)	ECM binding-laminin, fibronectin, TGF-β	ECM	8	24	.L.L.L.L.N-.I..-a.....					A40757
Decorin (human)	ECM binding-collagen, fibronectin, thrombospondin, TGF-β	ECM	10	24	.L.L.L.L.N-.I..-V.....					N8HUC8
Fibromodulin (bovine)	ECM binding-collagen, fibronectin	ECM	11	24	.L.L.L.L.N-.a..-a.....					S05390
Lumican (chicken)	Corneal transparency-?	ECM	12	24	.L.L.L.L.N-.L..-.....					A41748
Proteoglycan-Lb (chicken)	?-?	ECM	6	24	.L.a.L.N-.I.....					A41781
Osteoinductive factor (bovine)	Bone morphogenesis-BMP	ECM	6	24	.L.a.L.N-.a.....F...					A35272
Platelet GP Iba (human)	Cell adhesion-VWF, thrombin	PM (EC)	7	24	.L.L.L.L.N-.L..-LP.GL..L..					N8HUA
Platelet GP V (human)	Cell adhesion-GP IX, GP Ib	PM (EC)	14	24	.L.L.L.L.N-.L..-LP..LF..L..					-
YopM (Yersinia pestis)	Virulence factor-thrombin	IC + EC	12	20	.L.L.a.N-.L..-LP-....L-PP					A33950
IpaH7.8 (Shigella flexneri)	?-?	?	6	20	.L.L.V.N-.L..-LP-....L-P.					A35149
IpaH4.5 (Shigella flexneri)	?-?	?	8	20	.L.L.a.N-.L..-LP-....L-P.					S18248
Toll (Drosophila)	Embryo development-?	PM (EC)	19	24	.L.L.L.L.N-.L..-.....F...					A29943
Slit (Drosophila)	Axon development-?	EC	19	24	.L.L.L.L.N-.I.....F..L..					A36665
Connectin (Drosophila)	Synapse development-?	PM (EC)	7	24	.L.LNL.N-.I..-a..aF..L..					S28464
Choptin (Drosophila)	Photoreceptor-cell development-?	PM (EC)	30	24	.L.L.L.L.N-.a..-a..F..a..					A29944
Flightless-I (Drosophila)	Embryo development-?	PM (EC)	16	23	.L.L.LS.N-.L..-aP..a..L..					-
Oligodendrocyte myelin GP (human)	Myelination-?	PM (EC)	8	24	.L.L.LSN-.a..-a.....L..					A34210
CD14 (human)	Cell-surface receptor-LPS-LPB	PM (EC)	8	27	.a.L.L.L.N-.....					TDHUM4
Trk (human)	Receptor protein kinase-NGF	PM (EC)	2	23	.L.L.LS.N-.L..-.....					TVHUTT
TrkB (mouse)	Receptor protein kinase-BDNF, NT-3	PM (EC)	3	23	.L.L.aT.N-.LTS.....-T					S06943
TrkC (porcine)	Receptor protein kinase-NT-3	PM (EC)	3	23	.LR.aNLQN-.L...S.....					A40026
TMK1 (Arabidopsis thaliana)	Receptor protein kinase-?	PM (EC)	11	23	.L.a.L.N-.G.aP..-a.SL..					JQ1674
LHCG receptor (rat)	Signal transduction-LH, CG	PM (EC)	5	25	.L.L.a..T-.a.....F...					A41343
FSH receptor (rat)	Signal transduction-FSH	PM (EC)	7	25	.L.L.aS.T-.....LP...a..					A34548
TSH receptor (dog)	Signal transduction-TSH	PM (EC)	6	25	.a.L.a.NN-.a-S-a.....					A40077
Adenylate cyclase (Saccharomyces cerevisiae)	Signal transduction-RAS	PM (cytoplasm)	20	23	.L.L.L.N-.a..-a.....a.L..					OYBY
T-LR (Trypanosoma brucei)	?-?	?	18	23	.L.L.LSGC..a...-a..a.L..					A36359
RAD1 (Saccharomyces cerevisiae)	DNA repair-RAD10	Nucleus	3	23	.a.LaDI..N--LP..a.....N--					DB8YD1
RAD7 (Saccharomyces cerevisiae)	DNA repair-?	?	5	26	.L.L.a.C..a.....a.....P					A25226
DRT100 (Arabidopsis thaliana)	Recombination-?	Chloroplast	5	24	.L.LNL.N-.L.G.IP.S-a.S..					A46260
GRR1 (Saccharomyces cerevisiae)	Signal transduction-?	Cytoplasm	9	26	.L.a.L.C.NaTD..a..-L.L..					A41529
CCR4 (Saccharomyces cerevisiae)	Transcription-?	?	4	23	.L.L.a.N-.LT..-LP.E-a.....					S31286
sds22 (Schizosaccharomyces pombe)	Mitosis-dis2, sds21	Nucleus	11	22	.L.L.a.N-.I..-a--Ena..L..					A38439
p34 ribosome-binding protein (rat)	RM membranes-ribosome	RM membrane (cytoplasm)	4	24	.L.LDL.N-.L..-LP...F..L..					-
Carboxypeptidase N (human)	Stabilization-catalytic subunit	Plasma	12	24	.L.L.L.L.N-.L..-LP..aF..L..					A34901
Internalin (Listeria monocytogenes)	Invasion-?	Cell wall	13	22	NL..L.L.L.N-QISDI.P---L..L-T					A39930
InlB (Listeria monocytogenes)	?-?	?	6	22	.L.L.L.L.N-.L.DI....L..					C39930
LRR superfamily					5 10 15 20 25					
					.L..L.L.L.Na.a..aazaaazaaaz..					

Figure 3

>human DNA seq.

TAATACGACTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAA
TTCCCGGGTCGACCCACGCGTCCGTGGAGCGGAGCCAGGGTCTGAGCCTGCC
GGCTCATCCAGCCTCTCTTGCTGCCCTAGCGGCCTCCAACACAACCGCATCTG
GGAAATTGGAGCT:GACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATC
TTAGCTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCAC
TCCCTGGTCAAGCTGGACCTGACAGACAACCAGCTGACCACACTGCCCTGGC
TGGACTTGGGGGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCC
AGGCCTTCTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATG
CCTACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG
CAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGAGTCTTCAAAAAGGCC
CCTGGGCCTCCTTGCCAGACAAGCAGAGAACCCTATGACCAGGACCTGGATG
AGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCAGTGTCCAGTGTAGC
CCTACTCCAGGCCCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCAT
CCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGCTCTGCAATGGACTGG
TGCTGCTGACCGTGTTGCTGGCGGGCCTGCCCCCCTGCCCCCGGTCAAGTTT
GTGGTAGGTGCGATTGCAGGCGCCAACACCTTGACTGGCATTTCCTGTGGCCT
TCTAGCCTCAGTCGATGCCCTGACCTTTGGTCAGTTCTCTGAGTACGGAGCCC
GCTGGGAGACGGGGGCTAGGCTGCCGGGCCACTGGCTTCTGGCAGTACTTGG
GTCGGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCGAGTGCAGTGCAGCGTC
TCCGTCTCCTGTGTCCGGGCCATGCGGAAGTCCCCCTCCCTGGGCAGCGTTCCG
AGCAGGGGTCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCGCGCACTGCCC
CTGGCCTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGC
CACCTGAGGGTCAGCCAGCAGCCCTGGGCTTCACCGTGGCCCTGGTGATGAT
GAACTCCTTCTGTTTCTGGTCGTGGCCGGTGCCTACATCAAACCTGTACTGTGA
CCTGCCGCGGGGCGACTTTGAGGCCGTGTGGGACTGCGCCATGGTGAGGCAC
GTGGCCTGGCTCATCTTCGCAGACGGGCTCCTCTACTGTCCCGTGGCCTTCCT
CAGCTTCGCCTCCATGCTGGGCCTCTTCCCTGTCACGCCCGAGGCCGTCAAGT
CTGTCTGCTGGTGGTGCTGCCCTGCCTGCCTGCCTCAACCCACTGCTGTAC
CTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGGCTTCGGCCCCGCGC
AGGGGACTCAGGGCCCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGC
TCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTG
GAAGCTTCTGAAGCTGGGCGGCCCCCTGGGCTGGAGACCTATGGCTTCCCCTC
AGTGACCCTCATCTCCTGTCAGCAGCCAGGGGGCCCCCAGGCTGGAGGGCAGC
CATTGTGTAGAGCCAGAGGGGAACCACTTTGGGAACCCCCAACCTCCATGGA
TGGAGAACTGCTGCTGAGGGCAGAGGGATCTACGCCAGCAGGTGGAGGCTTG
TCAGGGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTTGCTTCACACGTGTA
AATATCCCTCCCCATTCTTCTTCCCCTCTCTTCCCTTTCCTCTCTCCCCCTCG
GTGAATGATGGCTGCTTCTAAAACAAATACAACCAAACTCAGCAGTGTGATCT
ATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCAT
CACCAACGGGTGCCTCTTGGCCTGGCTTTCCTTGGCCTTCCTCAGCTTCACCT
TGATACTGGGCCTCTTCCCTTGTATGTCTGAAGCTGTGGACCAGAGACCTGGAC
TTTTGTCTGCTTAAGGGAAATGAGGGAAGTAAAGACAGTGAAGGGGTGGAGGG
TTGATCAGGGCACAGTGGACAGGGAGACCTCACAGAGAAAGGCCTGGAAGGT
GATTTCCCGTGTGACTCATGGATAGGATACAAAATGTGTTCCATGTACCATTAAT
CTTGACATATGCCATGCATAAAGACTTCCTATTAAATAAGCTTTGGAAGAGATT
AAAAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGATCCAAGCTTACGTACGCGT
GCATGCGACGTCATAGCTCTTCTATAGTGTACCTAAATTCAATT

Figure 4

>fahr human

NTTHYRESWYACRYRSGIPGSTHASVERSQGLSLPAHPASLAALAASNTTASGKLE
DTFSQLSSLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTPLAGLGGLMHL
KLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDLHLD
DEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCEYL
FESWGIRLAVWAVLLSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCG
LLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSEASVLLLTLAAVQCSVSVS
CVRAYGKSPSLGSVRAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQP
AALGFTVALVMMNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAWLIFAD
GLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDL
RLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYG
FPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRLAEGSTPAGGGL
SGGGGFQPSGLAFASHV

Figure 5

LRR: domain 1 of 1, from 64 to 111: score 51.0, E = 2.6e-11

*->nLeeLdLsnNkLtslppgalsnLpnLeeLdLsnNnLtslppglfqnl

+L+ LdLs N ++s++p+a+s+L++L +LdL +N+Lt+lp + +L

fahr 64 SLQALDLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGL 110

k<-*

fahr 111 M 111

Figure 6

1 80
MISPELLALMCAVLCSAROGSDPOFGGRPACTAPCHQEDGIMLSADCEGLSVVENDLDELTAYLHRSNITE

81 160
IQGLFPHILFLENRLSGHLSHTPGQAFSGLSLKILMLQSNQLGTFPAELNELPSIQSLRLDANLISLWTFSEF

161 240
LSSRLHMLDNDALTEIPVRALNLPALQANTLAINHRIHPDYAFQNLTSVLVLEHNRICHVGTHSFEGLNLESLD

241 320
LWNYELQEFFLAIRTLGRLEGLCPHBNKAIPENAFBGNPLQTTHFYDNPIQFVGRSAPYLSKHLTLGNGATDIQE
~~-----~~
~~-----~~ NTHYRES WACKYRS GPGST

321 400
 FFDLGGTTSLEIATLTRAGIRLLPPGVQQLPRILILELSHQTEELPSLHRCQKLEIGLRRRIKETGADTFSQLGSL

 ---H-ASVE---PSQGLSLP---NHPASLAALASNTDAG-----KLEK-----DTPSLSL

401 480
QALDLSNATRAIDPEAFSTLHSLVKLDLTQNLTTPLAGLGGMHLKXGHLALSQAFSKDSFHLRILEVFPZYVOC
-----MHLKXGHLALSQAFSKDSFHLRILEVFPZYVOC-----
QALDLSNATRSIDPEAFSTLHSLVKLDLTQNLTTPLAGLGGMHLKXGHLALSQAFSKDSFHLRILEVFPZYVOC

481 560
 AYGTCASFFKTSQWQAEDFHPEZEEAPKRPGLGLLAGQAENHYDLQDQDQGTEDSKHPSPVQCSPTVGGFFKPCYHLE
 AYGTCASFFKTSQWQAEDFHPEZEEAPKRPGLGLLAGQAENHYDLQDQDQGTEDSKHPSPVQCSPTVGGFFKPCYHLE
 PYGCASFFKASGWEAETLHLDDESSKRPGLGLLAGQAENHYDQDLQDQDQGTEDSKHPSPVQCSPTVGGFFKPCYHLE

561 640
 SWGIRLAWAIVLVLVNLGLVLLTVFASGPSPLSPVKLVVGNMAGNALTGISQGLLASVDALTYGQFAEYGARHESG
 SWGIRLAWAIVLVLVNLGLVLLTVFASGPSPLSPVKLVVGNMAGNALSGISQGLLASVDALTYGQFAEYGARHESG
 SWGIRLAWAIVLVLVNLGLVLLTVFAGGPAPLPVVKTVVGNMAGNLTGESQGLLASVDALTYGQFSEYGARHETGL

641 I TM II 720
GQDMGFLAVLGSEASVLLTLAAVQCSISVTCVRAYGAPSPGSGVRAGAGCTALAGLAANPLASVGEYGASPICLFY
GQDMGFLAVLGSEASVLLTLAAVQCSISVTCVRAYGAPSPGSGVRAGAGCTALAGLAANPLASVGEYGASPICLFY
GCRMGFLAVLGSEASVLLTLAAVQCSVSVSCVRAYGKSPSLGSGVRAGVGLCTALAGLAANPLASVGEYGASPICLFY

721 TM III TM IV 800
 APPECPAALGFAVALVMMISLCFLVWAGAYIKLYCDLPRGOFZAWHDCAMVHVAMLI¹FA²DGLLYCPVA³IF⁴SPASH⁵IGL
 APPECPAALGFAVALVMMISLCFLVWAGAYIKLYCDLPRGOFZAWHDCAMVHVAMLI¹FA²DGLLYCPVA³IF⁴SPASH⁵IGL
 APPECPAALGFTVALVMMISLFCFLVWAGAYIKLYCDLPRGOFZAWHDCAMVHVAMLI¹FA²DGLLYCPVA³IF⁴SPASH⁵IGL

801 TMV TMVI 890
 FVTPPEAVKSVLLVWLPLPACINELLYLLENPHFDOLRLRLHPSRSPGFLAYAAANGELEKSSCDSTQALVAFSDVLI.
 FVTPPEAVKSVLLVWLPLPACINELLYLLENPHFDOLRLRLHPSRSPGFLAYAAANGELEKSSCDSTQALVAFSDVLI.
 FVTPPEAVKSVLLVWLPLPACINELLYLLENPHFDOLRLRLHPSRSPGFLAYAAANGELEKSSCDSTQALVAFSDVLI.

881 TM VI 980

EASEAGQPPGLETYGFPVSVTLISKHQFGATRLQGNHFVESDGTGTFGNQPPMKIGELLKARGATLAGCGSSVGGALNPSC
EASEAGQPPGLETYGFPVSVTLISKHQFGATRLQGNHFVESDGTGTFGNQPPMKIGELLKARGATLAGCGSSVGGALNPSC
EASEAGRPPGLETYGFPVSVTLISQQFGAPRLEGSHCVPEBGNHFGNQPQSMQIGELLKARGSTPAGGCLSGGGGQFQPSG

961	968
SLFASHLN	
SLFASHLN	
LAFASHVN	

Figure 7

G	L	H	N	L	E	T	L	D	L	N	Y	N	K	L	Q	E	F	P	V	20
GGG	CTG	CAC	AAT	CTG	GAG	ACA	CTA	GAC	CTG	AAT	TAT	AAC	AAG	CTG	CAG	GAG	TTC	CCT	GTG	60
A	I	R	T	L	G	R	L	Q	E	L	G	F	H	N	N	N	I	K	A	40
GCC	ATC	CGG	ACC	CTG	GGC	AGA	CTG	CAG	GAA	CTG	GGG	TTC	CAT	AAC	AAC	AAC	ATC	AAG	GCC	120
I	P	E	K	A	F	M	G	N	P	L	L	Q	T	I	H	F	Y	D	N	60
ATC	CCA	GAA	AAG	GCC	TTC	ATG	GGG	AAC	CCT	CTG	CTA	CAG	ACG	ATA	CAC	TTT	TAT	GAT	AAC	180
P	I	Q	F	V	G	R	S	A	F	Q	Y	L	P	K	L	H	T	L	S	80
CCA	ATC	CAG	TTT	GTG	GCA	AGA	TCG	GCA	TTC	CAG	TAC	CTG	CCT	AAA	CTC	CAC	ACA	CTA	TCT	240
L	N	G	A	M	D	I	Q	E	F	P	D	L	K	G	T	T	S	L	E	100
CTG	AAT	GGT	GCC	ATG	GAC	ATC	CAG	GAG	TTT	CCA	GAT	CTC	AAA	GGC	ACC	ACC	AGC	CTG	GAG	300
I	L	T	L	T	R	A	G	I	R	L	L	P	S	G	M	C	Q	Q	L	120
ATC	CTG	ACC	CTG	ACC	CGC	GCA	GGC	ATC	CGG	CTG	CTC	CCA	TCG	GGG	ATG	TGC	CAA	CAG	CTG	360
P	R	L	R	V	L	E	L	S	H	N	Q	I	E	E	L	P	S	L	H	140
CCC	AGG	CTC	CGA	GTC	CTG	GAA	CTG	TCT	CAC	AAT	CAA	ATT	GAG	GAG	CTG	CCC	AGC	CTG	CAC	420
R	C	Q	K	L	E	E	I	G	L	Q	H	N	R	I	W	E	I	G	A	160
AGG	TGT	CAG	AAA	TTG	GAG	GAA	ATC	GGC	CTC	CAA	CAC	AAC	CGC	ATC	TGG	GAA	ATT	GGA	GCT	480
D	T	F	S	Q	L	S	S	L	Q	A	L	D	L	S	W	N	A	I	R	180
GAC	ACC	TTC	AGC	CAG	CTG	AGC	TCC	CTG	CAA	GCC	CTG	GAT	CTT	AGC	TGG	AAC	GCC	ATC	CGG	540
S	I	H	P	E	A	F	S	T	L	H	S	L	V	K	L	D	L	T	D	200
TCC	ATC	CAC	CCT	GAG	GCC	TTC	TCC	ACC	CTG	CAC	TCC	CTG	GTC	AAG	CTG	GAC	CTG	ACA	GAC	600
N	Q	L	T	T	L	P	L	A	G	L	G	G	L	M	H	L	K	L	K	220
AAC	CAG	CTG	ACC	ACA	CTG	CCC	CTG	GCT	GGA	CTT	GGG	GGC	TTG	ATG	CAT	CTG	AAG	CTC	AAA	660
G	N	L	A	L	S	Q	A	F	S	K	D	S	F	P	K	L	R	I	L	240
GGG	AAC	CTT	GCT	CTC	TCC	CAG	GCC	TTC	TCC	AAG	GAC	AGT	TTC	CCA	AAA	CTG	AGG	ATC	CTG	720
E	V	P	Y	A	Y	Q	C	C	P	Y	G	M	C	A	S	F	F	K	A	260
GAG	GTG	CCT	TAT	GCC	TAC	CAG	TGC	TGT	CCC	TAT	GGG	ATG	TGT	GCC	AGC	TTC	TTC	AAG	GCC	780
S	G	Q	W	E	A	E	D	L	H	L	D	D	E	E	S	S	K	R	P	280
TCT	GGG	CAG	TGG	GAG	GCT	GAA	GAC	CTT	CAC	CTT	GAT	GAT	GAG	GAG	TCT	TCA	AAA	AGG	CCC	840
L	G	L	L	A	R	Q	A	E	N	H	Y	D	Q	D	L	D	E	L	Q	300
CTG	GGC	CTC	CTT	GCC	AGA	CAA	GCA	GAG	AAC	CAC	TAT	GAC	CAG	GAC	CTG	GAT	GAG	CTC	CAG	900
L	E	M	E	D	S	K	P	H	P	S	V	Q	C	S	P	T	P	G	P	320
CTG	GAG	ATG	GAG	GAC	TCA	AAG	CCA	CAC	CCC	AGT	GTC	CAG	TGT	AGC	CCT	ACT	CCA	GGC	CCC	960
F	K	P	C	E	Y	L	F	E	S	W	G	I	R	L	A	V	W	A	I	340
TTC	AAG	CCC	TGT	GAG	TAC	CTC	TTT	GAA	AGC	TGG	GGC	ATC	CGC	CTG	GCC	GTG	TGG	GCC	ATC	1020
V	L	L	S	V	L	C	N	G	L	V	L	L	T	V	F	A	G	G	P	360
GTG	TTG	CTC	TCC	GTG	CTC	TGC	AAT	GGA	CTG	GTG	CTG	CTG	ACC	GTG	TTC	GCT	GGC	GGG	CCT	1080
A	P	L	P	P	V	K	F	V	V	G	A	I	A	G	A	N	T	L	T	380
GCC	CCC	CTG	CCC	CCG	GTC	AAG	TTT	GTG	GTA	GGT	GCG	ATT	GCA	GGC	GCC	AAC	ACC	TTG	ACT	1140

FIGURE 8

G	I	S	C	G	L	L	A	S	V	D	A	L	T	F	G	Q	F	S	E	400
GGC	ATT	TCC	TGT	GGC	CTT	CTA	GCC	TCA	GTC	GAT	GCC	CTG	ACC	TTT	GGT	CAG	TTC	TCT	GAG	1200
Y	G	A	R	W	E	T	G	L	G	C	R	A	T	G	F	L	A	V	L	420
TAC	GGA	GCC	CGC	TGG	GAG	ACG	GGG	CTA	GGC	TGC	CGG	GCC	ACT	GGC	TTC	CTG	GCA	GTA	CTT	1260
G	S	E	A	S	V	L	L	L	T	L	A	A	V	Q	C	S	V	S	V	440
GGG	TCG	GAG	GCA	TCG	GTG	CTG	CTG	CTC	ACT	CTG	GCC	GCA	GTG	CAG	TGC	AGC	GTC	TCC	GTC	1320
S	C	V	R	A	Y	G	K	S	P	S	L	G	S	V	R	A	G	V	L	460
TCC	TGT	GTC	CGG	GCC	TAT	GGG	AAG	TCC	CCC	TCC	CTG	GGC	AGC	GTT	CGA	GCA	GGG	GTC	CTA	1380
G	C	L	A	L	A	G	L	A	A	A	L	P	L	A	S	V	G	E	Y	480
GGC	TGC	CTG	GCA	CTG	GCA	GGG	CTG	GCC	GCC	GCA	CTG	CCC	CTG	GCC	TCA	GTG	GGA	GAA	TAC	1440
G	A	S	P	L	C	L	P	Y	A	P	P	E	G	Q	P	A	A	L	G	500
GGG	GCC	TCC	CCA	CTC	TGC	CTG	CCC	TAC	GCG	CCA	CCT	GAG	GGT	CAG	CCA	GCA	GCC	CTG	GGC	1500
F	T	V	A	L	V	M	M	N	S	F	C	F	L	V	V	A	G	A	Y	520
TTC	ACC	GTG	GCC	CTG	GTG	ATG	ATG	AAC	TCC	TTC	TGT	TTC	CTG	GTC	GTG	GCC	GGT	GCC	TAC	1560
I	K	L	Y	C	D	L	P	R	G	D	F	E	A	V	W	D	C	A	M	540
ATC	AAA	CTG	TAC	TGT	GAC	CTG	CCG	CGG	GGC	GAC	TTT	GAG	GCC	GTG	TGG	GAC	TGC	GCC	ATG	1620
Y	R	H	V	A	W	L	I	F	A	D	G	L	L	Y	C	P	V	A	F	560
GTG	AGG	CAC	GTG	GCC	TGG	CTC	ATC	TTC	GCA	GAC	GGG	CTC	CTC	TAC	TGT	CCC	GTG	GCC	TTC	1680
L	S	F	A	S	M	L	G	L	F	P	V	T	P	E	A	V	K	S	V	580
GTC	AGC	TTC	GCC	TCC	ATG	CTG	GGC	CTC	TTC	CCT	GTC	ACG	CCC	GAG	GCC	GTC	AAG	TCT	GTC	1740
L	L	V	V	L	P	L	P	A	C	L	N	P	L	L	Y	L	L	F	N	600
CTG	CTG	GTG	GTG	CTG	CCC	CTG	CCT	GCC	TGC	CTC	AAC	CCA	CTG	CTG	TAC	CTG	CTC	TTC	AAC	1800
P	H	F	R	D	D	L	R	R	L	R	P	R	A	G	D	S	G	P	L	620
CCC	CAC	TTC	CGG	GAT	GAC	CTT	CGG	CGG	CTT	CGG	CCC	CGC	GCA	GGG	GAC	TCA	GGG	CCC	CTA	1860
A	Y	A	A	A	G	E	L	E	K	S	S	C	D	S	T	Q	A	L	V	640
GCC	TAT	GCT	GCG	GCC	GGG	GAG	CTG	GAG	AAG	AGC	TCC	TGT	GAT	TCT	ACC	CAG	GCC	CTG	GTA	1920
A	F	S	D	V	D	L	I	L	E	A	S	E	A	G	R	P	P	G	L	660
GCC	TTC	TCT	GAT	GTG	GAT	CTC	ATT	CTG	GAA	GCT	TCT	GAA	GCT	GGG	CGG	CCC	CCT	GGG	CTG	1980
E	T	Y	G	F	P	S	V	T	L	I	S	C	Q	Q	P	G	A	P	R	680
GAG	ACC	TAT	GGC	TTC	CCC	TCA	GTG	ACC	CTC	ATC	TCC	TGT	CAG	CAG	CCA	GGG	GCC	CCC	AGG	2040
L	E	G	S	H	C	V	E	P	E	G	N	H	F	G	N	P	Q	P	S	700
CTG	GAG	GGC	AGC	CAT	TGT	GTA	GAG	CCA	GAG	GGG	AAC	CAC	TTT	GGG	AAC	CCC	CAA	CCC	TCC	2100
M	D	G	E	L	L	L	R	A	E	G	S	T	P	A	G	G	G	L	S	720
ATG	GAT	GGA	GAA	CTG	CTG	CTG	AGG	GCA	GAG	GGA	TCT	ACG	CCA	GCA	GGT	GGA	GGC	TTG	TCA	2160
G	G	G	G	F	Q	P	S	G	L	A	F	A	S	H	V	*				737
GGG	GGT	GGC	GGC	TTT	CAG	CCC	TCT	GGC	TTG	GCC	TTT	GCT	TCA	CAC	GTG	TAA				2211
ATATCCCTCCCAATTCTTCTCTTCCCTCTCTTCCCTTTCCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAAAACA																				2290
AATACAACCAAAACTCAGCAGTGTGATCTATAGCAGGATGGCCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGA																				2369
CCATCACCAACGGGTGCCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACCTTGATACTGGGCCTCTTCCTTG																				2448
TCATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTTGTCTGCTTAAGGGAAATGAGGGAAAGTAAAGACAGTGAAGGGG																				2527

FIGURE 8
CONT.

FIGURE 8
CONT.

FIGURE 8
CONT.

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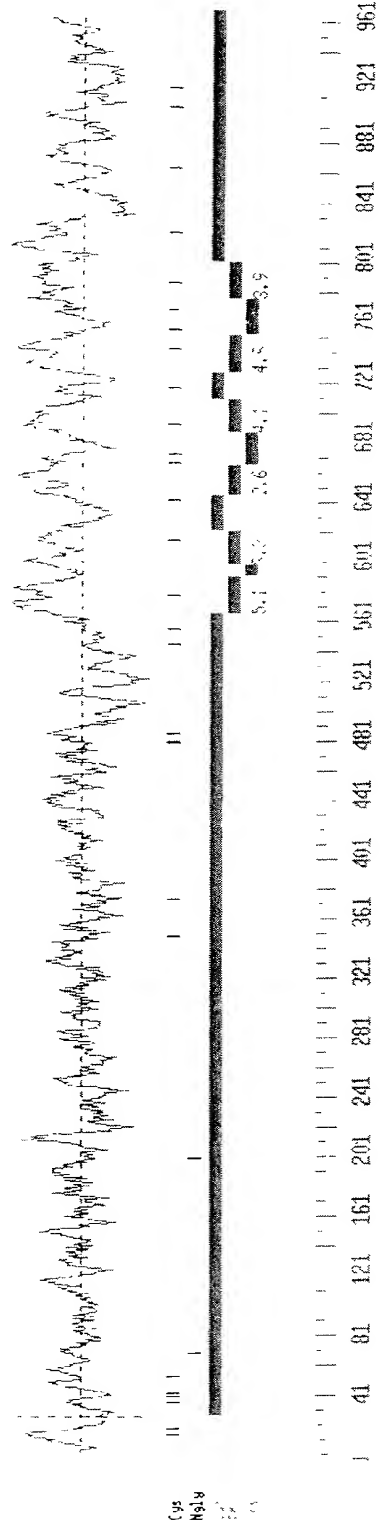


FIGURE 9

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.2/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.12184 seq

Query: 15088

Scores for sequence family classification (score includes all domains).

Model	Description	Score	E-value	N
LRR	Leucine Rich Repeat	241.4	1 3e-68	16
LRRNT	Leucine rich repeat N-terminal domain	27.2	0.00038	1
7tm_1	7 transmembrane receptor (rhodopsin family)	7.2	0.14	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
LRRNT	1/1	34	65	1	31	27.2	0.00038
LRR	1/16	67	90	1	23	12.4	11
LRR	2/16	91	114	1	23	24.2	0.0031
LRR	3/16	115	138	1	23	19.9	0.062
LRR	4/16	139	162	1	23	16.4	0.7
LRR	5/16	163	186	1	23	27.5	0.00031
LRR	6/16	187	210	1	23	12.1	13
LRR	7/16	211	234	1	23	21.6	0.019
LRR	8/16	235	257	1	23	18.2	0.2
LRR	9/16	258	281	1	23	19.0	0.11
LRR	10/16	282	305	1	23	10.2	32
LRR	11/16	306	328	1	23	5.6	1.5e+02
LRR	12/16	329	352	1	23	8.8	52
LRR	13/16	353	374	1	23	19.2	0.097
LRR	14/16	375	398	1	23	16.9	0.49
LRR	15/16	399	422	1	23	23.7	0.0042
LRR	16/16	423	446	1	23	16.4	0.66
7tm_1	1/2	635	662	51	79	3.4	2.2
7tm_1	2/2	784	827	207	259	1.1	11

Alignments of top-scoring domains:

LRRNT: domain 1 of 1, from 34 to 65: score 27.2, E = 0.00038

```
*->aCpreCtCsp..fglvVdCsgrgLtlevPrdIP<-*
aCp++C+C +++ I+ dCs++gL +vP dl
15088 34 ACPAPCHCQEEdgIMLSADCSELGLS-AVPGDLD 65
```

LRR: domain 1 of 16, from 67 to 90: score 12.4, E = 11

```
*->nLeeLdLsnN.LtspgglfsnLp<-*
+LdLs N+Lt+l pglf++L+
15088 67 LTAYLDLSMNnLTELPGLFHHLR 90
```

LRR: domain 2 of 16, from 91 to 114: score 24.2, E = 0.0031

```
*->nLeeLdLsnN.LtspgglfsnLp<-*
LeeL+Ls+N+L+++p +fs+L
15088 91 FLEELRLSGNhLSHIPGQAFSGLY 114
```

LRR: domain 3 of 16, from 115 to 138: score 19.9, E = 0.062

```
*->nLeeLdLsnN.LtspgglfsnLp<-*
+L+ L L+nN+L ++p +++ Lp
15088 115 SLKILMLQNNqLGGIPAEALWELP 138
```

LRR: domain 4 of 16, from 139 to 162: score 16.4, E = 0.7

```
*->nLeeLdLsnN.LtspgglfsnLp<-*
+L++L+L+ N ++ +p+ +f++L+
15088 139 SLQSLRLDANIISLVPERSFEGLS 162
```

LRR: domain 5 of 16, from 163 to 186: score 27.5, E = 0.00031

```
*->nLeeLdLsnN.LtspgglfsnLp<-*
+L++L+L++N Lt++p +++nLp
```

FIGURE 10

15088 163 SLRHLWLDDNaLTEIPVRALNNLP 186

LRR: domain 6 of 16, from 187 to 210: score 12.1, E = 13
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L+ L N+++++p+ +f+nL+
 15088 187 ALQAMTLALNriSHIPDYAFQNL 210

LRR: domain 7 of 16, from 211 to 234: score 21.6, E = 0.019
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +L+L+nN+++++l ++f++L
 15088 211 SLVVHLHNNriQHLGTHSFEG 234

LRR: domain 8 of 16, from 235 to 257: score 18.2, E = 0.2
 ->nLeeLdLsnN.LtslppglfsnLp<-
 nLe+LdL++N+L+++p +++ L
 15088 235 NLETLDLNYNkLQEFV-AIRTLG 257

LRR: domain 9 of 16, from 258 to 281: score 19.0, E = 0.11
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+eL ++nN+++ +p+++f + p
 15088 258 RLQELGFHNNkLAIPEKAFMG 281

LRR: domain 10 of 16, from 282 to 305: score 10.2, E = 32
 ->nLeeLdLsnN.LtslppglfsnLp<-
 L+++++ +N+++ + ++f+ Lp
 15088 282 LLQTIHFYDNpIQFVGRSAFYLP 305

LRR: domain 11 of 16, from 306 to 328: score 5.6, E = 1.5e+02
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L+L++ +++++p+ +++ +
 15088 306 KLHTLSLNGAmdIQEFPD--LKG 328

LRR: domain 12 of 16, from 329 to 352: score 8.8, E = 52
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Le L L + +++ lp+g +++Lp
 15088 329 SLEILTLTRAgIRLLPSGMCQQL 352

LRR: domain 13 of 16, from 353 to 374: score 19.2, E = 0.097
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L++L Ls+N+++++lp+ ++ ++
 15088 353 RLRVLELSHNqIEELPS--LHRC 374

LRR: domain 14 of 16, from 375 to 398: score 16.9, E = 0.49
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +Lee+ L++N+++ ++ ++fs+L+
 15088 375 KLEEIGLQHNNrWEIGADTFSQL 398

LRR: domain 15 of 16, from 399 to 422: score 23.7, E = 0.0042
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L+ LdLs N ++s++p++fs L
 15088 399 SLQALDLSWNaIRSIHPEAFSTL 422

LRR: domain 16 of 16, from 423 to 446: score 16.4, E = 0.66
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L +LdL +N+L+lp + +L
 15088 423 SLVKLDLTDNqLITLPLAGLGGLM 446

7tm_1: domain 1 of 2, from 635 to 662: score 3.4, E = 2.2
 ->dWpfGsalCkltaldivnmYaSillLta<-
 +W G ++C+ ++++ v+ + aS+llL+
 15088 635 RWETG-LGCRATGFLAVLGSEASV 662

7tm_1: domain 2 of 2, from 784 to 827: score 1.1, E = 11
 *->ICWIPyfiVllldtlc.lsiimsstCelervlptallvtwLayvNs
 I+ P +++ +l ++ ++++++v l++ ++
 15088 784 LLYCPVAFLSFASMLGIFPV-----TPEAVKSVLLVVLPLPA 820

cINPiY<-*
 cINP++Y
 15088 821 CLNPLLY 827

FIGURE 10 cont.

```
//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
-----
HMM file:                /ddm/robison/smart/smart/smart.all.hmms
Sequence file:           /prod/ddm/wspace/orfanal/oa-script.12184.seq
-----
```

Query: 15088

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
LRR_typ_2		247.2	2.3e-70	14
LRR_PS_2		78.1	1.8e-19	13
LRR_sd22_2		33.5	4.9e-06	5
lrrntl		25.7	0.0011	1
LRR_bac_2		11.8	3	7
LRR_RI_2		5.4	7.7	4

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
lrrntl	1/1	34	70	1	38	25.7	0.0011
LRR_PS_2	1/13	64	87	1	24	1.9	1.2e+02
LRR_typ_2	1/14	64	88	1	24	12.6	2.1
LRR_bac_2	1/7	89	108	1	20	0.9	80
LRR_PS_2	2/13	89	111	1	24	17.2	0.4
LRR_typ_2	2/14	89	112	1	24	32.1	1.3e-05
LRR_RI_2	1/4	89	115	1	28	3.6	14
LRR_bac_2	2/7	113	132	1	20	1.6	66
LRR_PS_2	3/13	113	136	1	24	1.1	1.5e+02
LRR_typ_2	3/14	113	136	1	24	19.2	0.1
LRR_bac_2	3/7	137	156	1	20	0.1	1e+02
LRR_PS_2	4/13	137	159	1	24	7.1	24
LRR_typ_2	4/14	137	160	1	24	25.9	0.00095
LRR_PS_2	5/13	161	183	1	24	11.4	6.6
LRR_typ_2	5/14	161	184	1	24	27.5	0.00031
LRR_sd22_2	1/5	161	187	1	22	5.3	31
LRR_RI_2	2/4	161	190	1	28	5.3	8
LRR_PS_2	6/13	185	207	1	24	7.0	25
LRR_typ_2	6/14	185	208	1	24	23.2	0.0062
LRR_PS_2	7/13	209	232	1	24	3.1	79
LRR_typ_2	7/14	209	232	1	24	28.1	0.0002
LRR_RI_2	3/4	209	235	1	28	1.2	31
LRR_sd22_2	2/5	209	235	1	22	13.5	3
LRR_bac_2	4/7	233	252	1	20	10.7	4.1
LRR_typ_2	8/14	233	255	1	24	16.1	0.76
LRR_PS_2	8/13	233	255	1	24	17.1	0.43
LRR_bac_2	5/7	256	275	1	20	0.2	1e+02
LRR_PS_2	9/13	256	278	1	24	2.9	85
LRR_typ_2	9/14	256	279	1	24	24.4	0.0026
LRR_typ_2	10/14	327	350	1	24	3.1	29
LRR_bac_2	6/7	351	370	1	20	14.6	1.3
LRR_PS_2	10/13	351	372	1	24	10.8	8
LRR_sd22_2	3/5	351	372	1	22	7.6	16
LRR_typ_2	11/14	351	373	1	24	18.8	0.13
LRR_RI_2	4/4	351	378	1	28	2.6	19
LRR_PS_2	11/13	373	396	1	24	2.3	1e+02
LRR_typ_2	12/14	374	396	1	24	6.8	10
LRR_sd22_2	4/5	397	418	1	22	7.0	19
LRR_PS_2	12/13	397	419	1	24	13.6	3.4
LRR_typ_2	13/14	397	420	1	24	30.4	4.3e-05
LRR_bac_2	7/7	421	440	1	20	5.8	18
LRR_sd22_2	5/5	421	441	1	22	3.7	49
LRR_PS_2	13/13	421	442	1	24	5.5	39
LRR_typ_2	14/14	421	444	1	24	21.6	0.018

Alignments of top-scoring domains:

FIGURE 11

lrrnt1: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtaVdCsgrglttleVpIdlPadttl<-
 +CPapC+C ++ ++ dCs++gL +vP dl + t +
 15088 34 ACPAPCHCQEdGIMLSADCELSLS--AVPGDLPLTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->LtsL.qvLdLsnNnLsGeIPsslgn<-
 L L+ +LdLs NnL+ e+ + l+
 15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFgg<-
 L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTTELQPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
 ->PpsLkeLnvsnNrLteLPeL<-
 +L+eL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLsHIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
 ->npsLreLdLsnNkl.gdeGaraLaeAlks<-
 ++ L+eL+Ls+N+l+++ G + ++L s
 15088 89 LRFLEELRLSGNHLsSHIPG--QAFSGLYS 115

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
 ->PpsLkeLnvsnNrLteLPeL<-
 sLk+L +nN+L P+
 15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G + l+
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L +L+ L L+nNqL +P++a++
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 psL++L+ + N ++ Pe
 15088 137 LPSLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
 15088 137 LPSLQSLRLDANLIS-LVPERSFE 159

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031

FIGURE 11 cont.

lrrntl: domain 1 of 1, from 34 to 70: score 25.7, E = 0.0011
 ->qCPapCtCsp.dfgtaVdCsgrgLttlevPldlPadttl<-
 +CPapC+C ++ ++ dCs+gL +vP dl + t +
 15088 34 ACPAPCHCQEdGIMLSADCSELGLS--AVPGDLDP LTAY 70

LRR_PS_2: domain 1 of 13, from 64 to 87: score 1.9, E = 1.2e+02
 ->LtsL.qvLdLsnNnLsGeIPsslgn<-
 L L+ +LdLs NnL+ e+ + l+
 15088 64 LDPLtAYLDLSMNNLT-ELQPGLFH 87

LRR_typ_2: domain 1 of 14, from 64 to 88: score 12.6, E = 2.1
 ->LpnL.reLdLsnNqLtsLPpgaFgg<-
 L L+ LdLs N+Lt+L pg+F++
 15088 64 LDPLtAYLDLSMNNLTQLPGLFHH 88

LRR_bac_2: domain 1 of 7, from 89 to 108: score 0.9, E = 80
 ->PpsLkeLnvsnNrLteLPeL<-
 +L+eL+ s+N+L+ P
 15088 89 LRFLEELRLSGNHLSHIPGQ 108

LRR_PS_2: domain 2 of 13, from 89 to 111: score 17.2, E = 0.4
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+ L++L+Ls+N+Ls +IP + ++
 15088 89 LRFLEELRLSGNHLs-HIPGQAFS 111

LRR_typ_2: domain 2 of 14, from 89 to 112: score 32.1, E = 1.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L+ L+eL+Ls+N+L+++P +aF+g
 15088 89 LRFLEELRLSGNHLSHIPGQAFSG 112

LRR_RI_2: domain 1 of 4, from 89 to 115: score 3.6, E = 14
 ->npsLreLdLsnNkl.gdeGaraLaeaLks<-
 ++ L+eL+Ls+N+L+++ G + ++L s
 15088 89 LRFLEELRLSGNHLsHIPG--QAFSGLYS 115

LRR_bac_2: domain 2 of 7, from 113 to 132: score 1.6, E = 66
 ->PpsLkeLnvsnNrLteLPeL<-
 sLk+L +nN+L P+
 15088 113 LYSLKILMLQNNQLGGIPAE 132

LRR_PS_2: domain 3 of 13, from 113 to 136: score 1.1, E = 1.5e+02
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L sL++L L+nN+L G + l+
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_typ_2: domain 3 of 14, from 113 to 136: score 19.2, E = 0.1
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 L +L+ L L+nNqL +P++a++
 15088 113 LYSLKILMLQNNQLGGIPAEALWE 136

LRR_bac_2: domain 3 of 7, from 137 to 156: score 0.1, E = 1e+02
 ->PpsLkeLnvsnNrLteLPeL<-
 psL++L+ + N ++ Pe
 15088 137 LPSLQSLRLDANLISLVPER 156

LRR_PS_2: domain 4 of 13, from 137 to 159: score 7.1, E = 24
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sLq+L+L N +s +P+ +
 15088 137 LPSLQSLRLDANLIS-LVPERSFE 159

LRR_typ_2: domain 4 of 14, from 137 to 160: score 25.9, E = 0.00095
 ->LpnLreLdLsnNqLtsLPpgaFgg<-
 Lp+L++L+L+ N ++ +P++ F+g
 15088 137 LPSLQSLRLDANLISLVPERSFEG 160

LRR_PS_2: domain 5 of 13, from 161 to 183: score 11.4, E = 6.6
 ->LtsLqvLdLsnNnLsGeIPsslgn<-
 L+sL++L L +N L+ eIP n
 15088 161 LSSLRHLWLDDNALT-EIPVRALN 183

LRR_typ_2: domain 5 of 14, from 161 to 184: score 27.5, E = 0.00031

FIGURE 11 cont.

```

*->LpnLreLdLsnNqLtsLPpgaFqg<-*
  L++Lr+L L++N+Lt++P +a+++
15088 161 LSSLRHLWLDNALTEIPVRALNN 184

LRR_sd22_2: domain 1 of 5, from 161 to 187: score 5.3, E = 31
*->LtnLeeLdLsqNkI....kkIENLde<-*
  L+ L++L+L +N +++ + + + NL
15088 161 LSSLRHLWLDNALteipvRALNNLPA 187

LRR_RI_2: domain 2 of 4, from 161 to 190: score 5.3, E = 8
*->npsLreLdLsnNklgdeGaraL..aeaLks<-*
  ++sLr L+L +N l++ +raL++ aL++
15088 161 LSSLRHLWLDNALTEIPVRALnnLPALQA 190

LRR_PS_2: domain 6 of 13, from 185 to 207: score 7.0, E = 25
*->LtsLqvLdLsnNnLsGeIPsslgn<-*
  L+ Lq L+ N++s +IP+ ++
15088 185 LPALQAMTLALNRIS-HIPDYAFQ 207

LRR_typ_2: domain 6 of 14, from 185 to 208: score 23.2, E = 0.0062
*->LpnLreLdLsnNqLtsLPpgaFqg<-*
  Lp+L+ L N++++P+ aFq+
15088 185 LPALQAMTLALNRISHIPDYAFQN 208

LRR_PS_2: domain 7 of 13, from 209 to 232: score 3.1, E = 79
*->LtsLqvLdLsnNnLsGeIPsslgn<-*
  LtsL+vL+L+nN++ s+
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_typ_2: domain 7 of 14, from 209 to 232: score 28.1, E = 0.0002
*->LpnLreLdLsnNqLtsLPpgaFqg<-*
  L++L +L+L+nN++++L F+g
15088 209 LTSLVVLHLHNNRIQHLGTHSFEG 232

LRR_RI_2: domain 3 of 4, from 209 to 235: score 1.2, E = 31
*->npsLreLdLsnNklgdeGaraLaeaLks<-*
  ++sL +L+L nN + G + e+L+
15088 209 LTSLVVLHLHNNRIQHLGTHSF-EGHNN 235

LRR_sd22_2: domain 2 of 5, from 209 to 235: score 13.5, E = 3
*->LtnLeeLdLsqNkI....kkIENLde<-*
  Lt L++L L +N+I++ +++++E+L++
15088 209 LTSLVVLHLHNNRIghlgtHSFEGLHN 235

LRR_bac_2: domain 4 of 7, from 233 to 252: score 10.7, E = 4.1
*->PpsLkeLnvsnNrLteLPeL<-*
  ++L++L+ ++N+L e+P
15088 233 LHNLETLDLNYNKLQEFPVA 252

LRR_typ_2: domain 8 of 14, from 233 to 255: score 16.1, E = 0.76
*->LpnLreLdLsnNqLtsLPpgaFqg<-*
  L+nL++LdL++N+L++ P + +
15088 233 LHNLETLDLNYNKLQEFPVAI-RT 255

LRR_PS_2: domain 8 of 13, from 233 to 255: score 17.1, E = 0.43
*->LtsLqvLdLsnNnLsGeIPsslgn<-*
  L++L++LdL++N+L e+P +
15088 233 LHNLETLDLNYNKLQ-EFPVAIRT 255

LRR_bac_2: domain 5 of 7, from 256 to 275: score 0.2, E = 1e+02
*->PpsLkeLnvsnNrLteLPeL<-*
  +L+eL+ nN+++ Pe
15088 256 LGRLQELGFHNNNIKAIPK 275

LRR_PS_2: domain 9 of 13, from 256 to 278: score 2.9, E = 85
*->LtsLqvLdLsnNnLsGeIPsslgn<-*
  L +Lq+L ++nNn+ IP+ +
15088 256 LGRLQELGFHNNNIK-AIPEKAFM 278

LRR_typ_2: domain 9 of 14, from 256 to 279: score 24.4, E = 0.0026
*->LpnLreLdLsnNqLtsLPpgaFqg<-*

```

FIGURE 11 cont.

15088 256 L+ L+eL +nN+++++P+ aF g
 LGR LQELGFHNNNIKA IPEKAFMG 279
 LRR_typ_2: domain 10 of 14, from 327 to 350: score 3.1, E = 29
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 ++L+ L L + ++ LP+g++q
 15088 327 TTSLEILT LTRAGIRLLPSGMCQQ 350
 LRR_bac_2: domain 6 of 7, from 351 to 370: score 14.6, E = 1.3
 ->PpsLkeLnvsnNrLteLPeL<-
 p+L+ L s+N+++eLP L
 15088 351 LPRLRVLELSHNQIEELPSL 370
 LRR_PS_2: domain 10 of 13, from 351 to 372: score 10.8, E = 8
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L++L+vL+Ls+N++ e+Ps l +
 15088 351 LPRLRVLELSHNQIE-ELPS-LHR 372
 LRR_sd22_2: domain 3 of 5, from 351 to 372: score 7.6, E = 16
 ->LtnLeeLdLsqNkikk1ENLde<-
 L +L++L+Ls+N+I+ + L+
 15088 351 LPRLRVLELSHNQIEELPSLHR 372
 LRR_typ_2: domain 11 of 14, from 351 to 373: score 18.8, E = 0.13
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 Lp Lr+L Ls+Nq+++LP + ++
 15088 351 LPRLRVLELSHNQIEELP-SLHRC 373
 LRR_RI_2: domain 4 of 4, from 351 to 378: score 2.6, E = 19
 ->npsLreLdLsnNklgdeGaralaealks<-
 +p+Lr+L Ls+N + + + ++ L++
 15088 351 LPRLRVLELSHNQIEELPSLHRCQKLEE 378
 LRR_PS_2: domain 11 of 13, from 373 to 396: score 2.3, E = 1e+02
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 +++L+++ L++N++ +++++
 15088 373 CQKLEEIGLQHNRIWEIGADTF SQ 396
 LRR_typ_2: domain 12 of 14, from 374 to 396: score 6.8, E = 10
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 +L+e L++N++ ++ +++F+
 15088 374 -QKLEEIGLQHNRIWEIGADTF SQ 396
 LRR_sd22_2: domain 4 of 5, from 397 to 418: score 7.0, E = 19
 ->LtnLeeLdLsqNkikk1ENLde<-
 L+ L+ LdLs+N I++i
 15088 397 LSSLQALDLSWNAIRSIHPEAF 418
 LRR_PS_2: domain 12 of 13, from 397 to 419: score 13.6, E = 3.4
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sLq LdLs+N + +I ++ ++
 15088 397 LSSLQALDLSWNAIR-SIHPEAFS 419
 LRR_typ_2: domain 13 of 14, from 397 to 420: score 30.4, E = 4.3e-05
 ->LpnLreLdLsnNqLtsLPpgaFqg<-
 L++L+ LdLs+N+++s++p+aF+
 15088 397 LSSLQALDLSWNAIRSIHPEAFST 420
 LRR_bac_2: domain 7 of 7, from 421 to 440: score 5.8, E = 18
 ->PpsLkeLnvsnNrLteLPeL<-
 +sL +L+ +N+Lt+LP
 15088 421 LHS LVKLDLTDNQLTTLPLA 440
 LRR_sd22_2: domain 5 of 5, from 421 to 441: score 3.7, E = 49
 ->LtnLeeLdLsqNkikk1ENLde<-
 L+ L+ LdL +N+++ + L +
 15088 421 LHS LVKLDLTDNQLTTL-PLAG 441
 LRR_PS_2: domain 13 of 13, from 421 to 442: score 5.5, E = 39
 ->LtsLqvLdLsnNnLsGeIPsslgN<-
 L+sL+ LdL +N+L+ ++P g

FIGURE 11 cont.

```

15088  421  LHSLVKLDLTDNQLT~TLPL~AGL  442
LRR_typ_2: domain 14 of 14, from 421 to 444: score 21.6, E = 0.018
          *->LpnLreLdlsnNqLtsLPpqaFqg<-*
          L++L +LdL +NqLt+LP  ++g
15088  421  LHSLVKLDLTDNQLTTPLAGLG  444
//

```

FIGURE 11 cont.

GAP of: FrGcgManager_101_HTAUB3ha_ check: 2817 from: 1 to: 3637

mLGR6 - 1 (analysis only) - Import - complete

to: FrGcgManager_101_ITA0fLsO_ check: 3059 from: 1 to: 2711

corrected human LGR6 (analysis o - Import - complete

Symbol comparison table:

/ddm_local/gcg/gcg_9.1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight: 12 Average Match: 10.000
Length Weight: 4 Average Mismatch: 0.000

Quality: 21826 Length: 3688
Ratio: 8.051 Gaps: 20
Percent Similarity: 84.248 Percent Identity: 84.211

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

FrGcgManager_101_HTAUB3ha_ x FrGcgManager_101_ITA0fLsO_

901 CCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAACTAT 950 MOUSE
1GGGCTGCACAATCTGGAGACACTAGACCTGAATTAT 36 HUMAN
951 AATGAGCTGCAGGAGTTCCCTTGGCTATCCGGACCCTGGGCAGACTGCA 1000
37 AACAGCTGCAGGAGTTCCCTGTGGCCATCCGGACCCTGGGCAGACTGCA 86
1001 AGAATTGGGTTTCCATAACAACAACATCAAGGCTATCCCAGAGAAAGCCT 1050
87 GGAAGCTGGGTTTCCATAACAACAACATCAAGGCCATCCCAGAAAAGCCT 136
1051 TCATGGGCAACCCCTCTCCTGCAGACAATACATTTTTATGACAACCCAATC 1100
137 TCATGGGGAACCCCTCTGCTACAGACGATACACTTTTATGATAACCCAATC 186
1101 CAGTTTGTGGGAAGGTCAGCATTCCAGTACCTGTCTAAACTGCATACGCT 1150
187 CAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAAACTCCACACACT 236
1151 ATCTTTGAATGGTGCCACTGATATCCAAGAGTTCCCAGACCTCAAAGGCA 1200
237 ATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGGCA 286
1201 CCACTAGCCTGGAGATCCTGACCCTGACCCGTGCGGGCATCAGACTGCTC 1250
287 CCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTC 336
1251 CCACCGGGAGTGTGCCAACAGCTGCCTAGGCTCCGAATCCTGGAGCTGTC 1300
337 CCATCGGGGATGTGCCAACAGCTGCCCAGGCTCCGAGTCCTGGAAGTGTG 386

FIGURE 12

1301 TCATAATCAGATCGAGGAGTTACCCAGCCTGCACAGATGTCAGAAGCTGG 1350
 ||| ||||| || ||||| | ||||| ||||| ||||| |||
 387 TCACAATCAAATTGAGGAGCTGCCCAGCCTGCACAGGTGTCAGAAATTGG 436

1351 AGGAAATTGGCCTCCGACATAACAGGATCAAGGAAATTGGTGCAGATACC 1400
 ||||| ||||| ||| ||| | ||| ||||| || |||||
 437 AGGAAATCGGCCTCCAACACAACCGCATCTGGGAAATTGGAGCTGACACC 486

1401 TTCAGCCAGCTGGGCTCCTTGCAAGCTTTAGACCTGAGTTGGAATGCCAT 1450
 ||||| ||||| ||||| ||||| | ||| || ||||| |||||
 487 TTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAGCTGGAACGCCAT 536

1451 CCGTGCCATCCACCCTGAGGCTTTCTCAACCCTTCGATCCTTGGTTAAGC 1500
 ||| ||||| ||||| ||||| ||||| | ||| ||||| |||||
 537 CCGGTCCATCCACCCTGAGGCTTCTCCACCCTGCACTCCCTGGTCAAGC 586

1501 TGGACCTGACTGACAACCAGCTGACCACACTGCCCCCTGGCTGGGCTGGGA 1550
 ||||| ||||| ||||| ||||| ||||| ||||| || |||||
 587 TGGACCTGACAGACAACCAGCTGACCACACTGCCCCCTGGCTGGACTTGGG 636

1551 GGCCTGATGCACCTGAAGCTCAAAGGGAACCTTGGCCCTGTCTCAGGCCTT 1600
 ||| ||||| ||||| ||||| ||||| | ||| || ||||| |||||
 637 GGCTTGATGCATCTGAAGCTCAAAGGGAACCTTGCTCTCTCCAGGCCTT 686

1601 CTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCCTACGCCT 1650
 ||||| ||||| ||||| ||||| ||||| ||||| || |||||
 687 CTCCAAGGACAGTTTCCCAAACTGAGGATCCTGGAGGTGCCTTATGCCT 736

1651 ACCAGTGCTGTGCCCTACGGCATCTGTGCCAGCTTCTTCAAGACCTCTGGG 1700
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 737 ACCAGTGCTGTCCCTATGGGATGTGTGCCAGCTTCTTCAAGGCCTCTGGG 786

1701 CAGTGGCAGGCCGAGGACTTTCATCCAGAAGAAGAGGAGGCACCAAAGAG 1750
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 787 CAGTGGGAGGCTGAAGACCTTACCTTGATGATGAGGAGTCTTCAAAAAG 836

1751 GCCCCCTGGGTCTCCTTGCTGGACAAGCTGAGAACCCTATGACCTAGACC 1800
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 837 GCCCCCTGGGCCTCCTTGCCAGACAAGCAGAGAACCCTATGACCAGGACC 886

1801 TGGATGAGCTCCAGATGGGGACAGAGGACTCAAAGCCAAACCCAGTGTC 1850
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 887 TGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCAGTGTC 936

1851 CAGTGCAGCCCTGTTCCAGGCCCTTCAAGCCCTGCGAGCACCTCTTTGA 1900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 937 CAGTGTAGCCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGA 986

1901 GAGCTGGGGCATCCGCCTTGCTGTGTGGGCCATCGTGCTGCTCTCCGTAC 1950
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 987 AAGCTGGGGCATCCGCCTGGCCGTGTGGGCCATCGTGTTGCTCTCCGTGC 1036

1951 TCTGTAACGGGCTGGTGCTGCTGACAGTCTTTGCCAGCGGACCCAGCCCCG 2000
 |||| || || ||||| ||||| || ||||| ||||| |||||
 1037 TCTGCAATGGACTGGTGCTGCTGACCGTGTTGCTGGCGGGCCTGCCCCC 1086

2001 CTGTCCCCCGTCAAGCTTGTGGTGGGTGCGATGGCAGGCGCCAACGCCCT 2050
 ||| |||| ||||| ||||| ||||| ||||| ||||| |||||
 1087 CTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAGGCGCCAACACCTT 1136

FIGURE 12

CONT.

2801 GAAGAGCTCCTGCGACTCCACCCAAGCGCTGGTGGCTTTCTCAGATGTGG 2850
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1887 GAAGAGCTCCTGTGATTCTACCCAGGCCCTGGTAGCCTTCTCTGATGTGG 1936
 2851 ATCTTATTCTGGAAGCTTCTGAGGCTGGGCAGCCTCCTGGGCTAGAGACC 2900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1937 ATCTCATTCTGGAAGCTTCTGAAGCTGGGCGGCCCTGGGCTGGAGACC 1986
 2901 TATGGCTTCCCTTCAGTGACCCTCATCTCCCGACATCAGCCGGGGGCCAC 2950
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1987 TATGGCTTCCCCTCAGTGACCCTCATCTCCTGTCAGCAGCCAGGGGCCCC 2036
 2951 CAGGCTGGAGGGAAACCATTTTATAGAGTCTGATGGAACCAAGTTTGGGA 3000
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2037 CAGGCTGGAGGGCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGGGA 2086
 3001 ACCCACAACCTCCCATGAAGGGGAGAACTGCTGCTGAAGGCAGAGGGAGCC 3050
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2087 ACCCCCAACCTCCATGGATGGAGAACTGCTGCTGAGGGCAGAGGGATCT 2136
 3051 ACTTTGGCAGGCTGTGGCTCTTCCGTGGGTGGAGCCCTCTGGCCCTCTGG 3100
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2137 ACGCCAGCAGGTGGAGGCTTGTGAGGGGTGGCGGCTTTCAGCCCTCTGG 2186
 3101 CTCTCTCTTTGCCTCTCACTTGTAATATCCCT..... 3133
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2187 CTTGGCCTTTGCTTCACACGTGTAATATCCCTCCCCATTCTTCTCTTCC 2236
 3134 .CTCTGTT...TGTC..CTCTCCCCATC...CAATGATGGCTGCTTATAA 3174
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2237 CCTCTCTTCCCTTTCTCTCTCCCCCTCGGTGAATGATGGCTGCTTCTAA 2286
 3175 AAGAAAGACAACCTCCAAC.....TCCATAGCAAGATGGCCAAC 3212
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2287 AACAAATACAACCAAACTCAGCAGTGTGATCTATAGCAGGATGGCCAG 2336
 3213 ACCTCTGACTCCATTGTT...CTCTCTCCACGACCCCTAACCAATGAGTG 3259
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2337 TAC.CTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGTG 2385
 3260 CTTCCAAGTCTTGCTTTGTCTTGGCCT...TCAGCTTCACTTTCACCCTG 3306
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2386 CCTCTTGGCCTGGCTTTCCCTTGGCCTTCCTCAGCTTCACTTGATACTG 2435
 3307 GGC..CTTCTCTGTCCAATCCAATACTTCTGA.CAGAGGCCTGGGAAATT 3353
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2436 GGCCTCTTCCTTGTGATGTCTGAAGCTGTGGACCAGAGACCTGGACTTTT 2485
 3354 ...TGCATAGGAGAAAGGAGAAAAGCAAAAGACAGTGAAGGTTATTGGGC 3400
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2486 GTCTGCTTAAGGGAAATGAGGGAAG.TAAAGACAGTGAAG.....GGG. 2527
 3401 CCTGACAGAGCCATGATCAGTAAGTGCAGAGT.GATGGGGAGGTCTCACA 3449
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2528 ..TG...GAGGGTTGATC....AGGGCACAGTGGACAGGGAGACCTCACA 2568
 3450 GAGCATGACACTGGAAGACAACCTACCAAAGACATTGGAGAGTCTCCCCTG 3499
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 2569 GAGAAAGGC.CTGAAGGTGATTTCC.....CGTGTGACTC..... 2603

FIGURE 12

CONT.


```

>15088
> Fbh150881 - Import - vector trimmed
CCGCCSGCGGTGCAGCCCGCCGGGACCGGGAGGCGGCAGCTGCGGCCACCGCGCCCGTGCG
TCCGCGCCCGGCCGCCAGGTGCCCCAGTAGCCCGACCGCCGAGATGCCAGCCCGCCGGG
GCTCCGGGGCGCTATGGCTTTGCGCCGCGCTGTGCGCTTCCCGGAGGGCCGGCGCGCCCG
CCAGCCCGGCCCGGGGCCACCGCTGCCCGGCCCTGCCACTGCCAGGAGGACGGCAT
CATGCTGTCTGCCGACTGCTCTGAGCTCGGGCTGTCCGCCGTTCCGGGGGACCTGGACCC
CCTGACGGCTTACCTGGACCTCAGCATGAACAACCTCACAGAGCTTCAGCCTGGCCTCTT
CCACCACCTGCGCTTCTTGGAGGAGCTGCGTCTCTCTGGGAACCATCTCTCACACATCCC
AGGACAAGCATTCTCTGGTCTCTACAGCCTGAAAATCCTGATGCTGCAGAACAATCAGCT
GGGAGGAATCCCCGAGAGGCGCTGTGGGAGCTGCCGAGCCTGCAGTCGCTGCGCCTAGA
TGCCAACCTCATCTCCCTGGTCCCGGAGAGGAGCTTTGAGGGGCTGTCTCCCTCCGCCA
CCTCTGGCTGGACGACAATGCACTACGGAGATCCCTGTACAGGCCCTCAACAACCTCCC
TGCCCTGCAGGCCATGACCCTGGCCCTCAACCGCATCAGCCACATCCCCGACTACGCGTT
CCAGAATCTCACCAGCCTTGTGGTGTGCATTTGCATAACAACCGCATCCAGCATCTGGG
GACCCACAGCTTCGAGGGGCTGCACAATCTGGAGACACTAGACCTGAATTATAACAAGCT
GCAGGAGTTCCCTGTGGCCATCCGGACCTGGGCAGACTGCAGGAACCTGGGTTCCATAA
CAACAACATCAAGGCCATCCAGAAAAGGCCCTTCATGGGGAACCTCTGTACAGACGAT
ACACTTTTATGATAACCCAATCCAGTTTGTGGGAAGATCGGCATTCCAGTACCTGCCTAA
ACTCCACACACTATCTCTGAATGGTGCCATGGACATCCAGGAGTTTCCAGATCTCAAAGG
CACCACCAGCCTGGAGATCCTGACCCTGACCCGCGCAGGCATCCGGCTGCTCCCATCGGG
GATGTGCCAACAGCTGCCAGGCTCCGAGTCCCTGGAACGTGTCTCACAATCAAATTGAGGA
GCTGCCAGCCTGCACAGGTGTGAGAAATGGAGGAAATCGGCCTCCAACACAACCGCAT
CTGGGAAATTTGGAGCTGACACCTTCAGCCAGCTGAGCTCCCTGCAAGCCCTGGATCTTAG
CTGGAACGCCATCCGGTCCATCCACCCTGAGGCCTTCTCCACCCTGCACTCCCTGGTCAA
GCTGGACCTGACAGACAACCACTGACCACACTGCCCTGGCTGGACTTGGGGGCTTGAT
GCATCTGAAGCTCAAAGGGAACCTTGTCTCTCCAGGCCTTCTCCAAGGACAGTTTCCC
AAAAGTGAAGATCCTGGAGTGCCCTTATGCCATACCAGTGTCTGTCCCTATGGGATGTGTG
CAGCTTCTTCAAGGCCTCTGGGCGAGTGGGAGGCTGAAGACCTTCACCTTGATGATGAGGA
GTCTTCAAAAAGGCCCTCGGGCTCCTTGCCAGACAAGCAGAGAACCCTATGACCAGGA
CCTGGATGAGCTCCAGCTGGAGATGGAGGACTCAAAGCCACACCCCACTGTCCAGTGAG
CCCTACTCCAGGCCCTTCAAGCCCTGTGAGTACCTCTTTGAAAGCTGGGGCATCCGCCT
GGCCGTGTGGGCCATCGTGTGCTCTCCGTGCTCTGCAATGGAAGTGGTGTGCTGACCGT
GTTGCTGTGCGGGCCTGCCCCCTGCCCCCGGTCAAGTTTGTGGTAGGTGCGATTGCAAG
CGCCAACACCTTGAATGGCATTCTGTGGCCTTCTAGCCTCAGTCGATGCCCTGACCTT
TGGTCAAGTTCTCTGAGTACGGAGCCCGCTGGGAGACGGGGCTAGGCTGCCGGGCCACTGG
CTTCTGGCAGTACTTGGGTGCGAGGCATCGGTGCTGCTGCTCACTCTGGCCGCACTGCA
GTGACGCGTCTCCGTCTCCTGTGTCCGGGCTATGGGAAGTCCCCCTCCCTGGGCAGCGT
TCGAGCAGGGGTCCTAGGCTGCCTGGCACTGGCAGGGCTGGCCGCCGCACTGCCCTGGC
CTCAGTGGGAGAATACGGGGCCTCCCCACTCTGCCTGCCCTACGCGCCACCTGAGGGTCA
GCCAGCAGCCCTGGGCTTACCGTGGCCCTGGTGTATGATGAACCTCTTCTGTTTCTGGT
CGTGGCCGGTGCCATCAAACTGTACTGTGACCTGCCGCGGGGCGACTTTGAGGCCGT
GTGGGACTGCGCCATGGTGAGGCACGTGCCCTGGCTCATCTTCGACAGACGGGCTCCTCTA
CTGTCCCGTGGCCTTCTCAGCTTCGCCTCCATGCTGGGCTCTTCCCTGTACGCCCCGA
GGCCGTCAAGTCTGTCTGTGCTGGTGGTGTGCCCTGCCTGCCTCAACCCCACTGCT
GTACCTGCTCTTCAACCCCCACTTCCGGGATGACCTTCGGCGGCTTCGGCCCGCGCAGG
GGACTCAGGGGCCCTAGCCTATGCTGCGGCCGGGGAGCTGGAGAAGAGCTCCTGTGATTG
TACCCAGGCCCTGGTAGCCTTCTCTGATGTGGATCTCATTCTGGAAGCTTCTGAAGCTGG
GCGGCCCTGGGCTGGAGACCTATGGCTTCCCTCAGTGACCCCTCATCTCCTGTGAGCA
GCCAGGGGCCCCAGGCTGGAGGCCAGCCATTGTGTAGAGCCAGAGGGGAACCACTTTGG
GAACCCCAACCCCTCATGGATGGAGAAGTCTGCTGAGGGCAGAGGGATCTACGCCAGC
AGGTGGAGGCTTGTGAGGGGTGGCGGCTTTCAGCCCTCTGGCTTGGCCTTGTCTTCA
CGTGTAAATATCCCTCCCCATTTCTCTTCCCTCTCTTCCCTTCTCTCCCCCTC
GGTGAATGATGGCTGCTTCTAAACAAATAACAACAAAACCTCAGCAGTGTGATCTATAGC
AGGATGGCCAGTACCTGGCTCCACTGATCACCTCTCTCCTGTGACCATCACCAACGGGT
GCCTCTTGGCCTGGCTTTCCCTTGGCCTTCTCAGCTTCACCTTGATACTGGGCCTCTTC
CTTGTGATGTCTGAAGCTGTGGACCARAGACCTGGACTTTTGTCTGCTTAAGGGAAATGA
GGGAAGTAAAGACAGTGAAGGGGTGGAGGGTTGATCAGGGCACAGTGGACAGGGAGACCT
CACARAAAAAGGCCTGGAAGGKGATTTCCCGTGTGACTCATGGRTAGGAWACAAAATGTG
TTCCATGTACCAATTAATCTTGACATATGCCATGCATAAARACTTCTATTAAATAAGCT
TTGGRAGAGATT

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FIGURE 14

>15088

MPSPPLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSADCSELGLSAVPGDLDPLTAYLDLSMNNLT
ELQPLGFHHLRFLEELRLSGNHLSHIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
SLRHLWDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSVLVHLHNNRIQHLGTHSFEGHNLLETDLNYNK
LQEFPAIRTLGRLQELGFHNNNIKAPEKAIFMGNPLLQTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFDLKGTT
SLEILTLTRAGIRLLPSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQALDLSWNAIR
SIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFCKASG
QWEAEDLHLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPGPFKPCYLFESWGIRLAWWAIVL
LSVLCNGLVLLTVFAGGPAPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAVLGSE
ASVLLTLAAVQCSVSVSCVRAVGKSPSLGSRVAGVLGCLALAGLAAALPLASVGEYGASPLCLPYAPPEGQPAALGFTVA
LVMMNSFCFLVAGAYIKLYCDLPRGDFEAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVL
PLPACLNPLLYLLFNPHFRDDLRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFP
SVTLISCQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGLSGGGGFQPSGLAFASHV*

FIGURE 15

protein alignment between mouse and human
> LGR6.

15088m(analysis only) - Import - complete

to: FrGcgManager_9_QBAsD4iW_ check: 8637 from: 1 to: 968

15088h(analysis only) - Import - complete

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/BLOSUM62

CompCheck: 1102

Matrix made by matblas from blosum62.iij

Gap Weight:	12	Average Match:	2.778
Length Weight:	4	Average Mismatch:	-2.248

Quality:	4495	Length:	968
Ratio:	4.653	Gaps:	2
Percent Similarity:	91.097	Percent Identity:	89.855

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

FrGcgManager_9_PBA0KgkFJ x FrGcgManager_9_QBAsD4iW_ March 15, 19101 15:24

```
1  MHSPPGLLALWLCASARGGSDPQPGPGRPACPAPCHCQEDGIMLSA 50  Mouse
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1  MPSPPGLRALWLCAALCASRRAGGAPQPGPGPTACPAPCHCQEDGIMLSA 50  Human

51  DCSSELGLSVVPADLDPLTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGN 100
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51  DCSSELGLSAVPGDLDPLTAYLDLSMNNLTQLPGLFHHLRFLEELRLSGN 100

101  HLSHIPGQAFSGLHSLKIIMLQSNQLRGIPAEALWELPSLQSLRLDANLI 150
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101  HLSHIPGQAFSGLYSLKIIMLQNNQLGGIPAEALWELPSLQSLRLDANLI 150

151  SLVPERSFEGLSRLHLWLDNALTEIPVRALNNLPALQAMTLALNHIRH 200
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
151  SLVPERSFEGLSRLHLWLDNALTEIPVRALNNLPALQAMTLALNRISH 200

201  IPDYAFQNLTSLVVLHLHNNRIQHVGTHSFEGLHNLETLDLNYNELQEF 250
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
201  IPDYAFQNLTSLVVLHLHNNRIQHLGTHNFEGLHNLEPLDLNYNKLQEF 250

251  LAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300
|  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
251  VAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLLQTIHFYDNPIQFVGRSA 300

301  FQYLSKLHTLSLNGATDIQEFDDLKGTTSLEILTLTRAGIRLLPPGVCQQ 350
|  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
301  FQYLPKLHTLSLNGAMDQEFDDLKGTTSLEILTLTRAGIRLLPSGMCQQ 350
```

FIGURE 16

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351 LPRLRILELSHNQIEELPSLHRCQKLEEIGLRHNRIKEIGADTFSQLGSL 400
      |||||:|||||
351 LPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLGSL 400
      .
401 QALDLSWNAIRAIHPEAFSTLRSVLKDLTDNQLTTPLAGLGGLMHLKL 450
      |||||
401 QALDLSWNAIRSIHPEAFSTLRSVLKDLTDNQLTTPLAGLGGLMHLKL 450
      .
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCAYGICASFFKTSQGWQAEDF 500
      |||||
451 KGNLALSQAFSKDSFPKLRILEVPYAYQCCPYGMCASFFKASGQWEAEDL 500
      .
501 HPEEEEEAPKRPLGLLAGQAENHYDLDLDELQMGTEDSKPNSVQCSVPVG 550
      |::||
501 HLDDEESSKRPLGLLARQAENHYDQDLDELQLEMEDSKPHPSVQCSPTPG 550
      .
551 PFKPCEHLFESWGIRLAVWAIVLLSVLCNG.VLLTVFASGPSPLSP.KLV 598
      |||||:|||||
551 PFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVLLTVFAGGPAPLPVKFV 600
      .
599 VGAMAGANALTGISCGLLASVDALTYGQFAEYGARWESGLGCQATGFLAV 648
      |||.|||
601 VGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCRATGFLAV 650
      .
649 LGSEASVLLLTAAVQCSISVTCVRAYGKAPSGSVRAGALGCLALAGLA 698
      |||||:|||
651 LGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLA 700
      .
699 AALPLASVGEYGASPLCLPYAPPEGRPAALGFAVALVMMNSLCFLVVAGA 748
      |||||
701 AALPLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGA 750
      .
749 YIKLYCDLPRGDFAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 798
      |||||
751 YIKLYCDLPRGDFAVWDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGL 800
      .
799 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLWPSRSPGP 848
      |||||
801 FPVTPEAVKSVLLVVLPLPACLNPLLYLLFNPHFRDDLRLRLRPRAGDSGP 850
      .
849 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGQPPGLETYGFPSVT 898
      |||||
851 LAYAAAGELEKSSCDSTQALVAFSDVDLILEASEAGRPPGLETYGFPSVT 900
      .
899 LISRHQPGATRLEGNHFIESDGTKFGNPQPPMKGELLKAEATLAGCGS 948
      ||| ||| |||||.| :| :| ||||| | ||||:|||.| |||
901 LISQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGSTPAGGGL 950
      .
949 SVGGALWPSGSLFASHL* 966
      ||| ||| |||||.
951 SGGGGFQPSGLAFASHV* 968

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FIGURE 16 cont.